



# results of BLAST

## BLASTP 2.2.4 [Aug-26-2002]

### Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1038413121-06030-16900

### Query=

(10 letters)

Database: All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PFF

1,243,428 sequences; 395,713,720 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

No significant similarity found. For reasons why, [click here](#).

Database: All non-redundant GenBank CDS  
translations+PDB+SwissProt+PIR+PFF

Posted date: Nov 25, 2002 10:56 PM

Number of letters in database: 395,713,720

Number of sequences in database: 1,243,428

Lambda	K	H
0.321	0.134	0.465

### Gapped

Lambda	K	H
0.267	0.0410	0.149

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 0,402,725

Number of Sequences: 1243428

Number of extensions: 35341

Number of successful extensions: 2

Number of sequences better than 10.0: 0

Number of HSP's better than 10.0 without gapping: 0

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 2

Number of HSP's gapped (non-prelim): 0

length of query: 10

length of database: 395,713,720

effective HSP length: -

effective length of query: 24

effective length of database: 395,713,720

effective search space: 9497129280  
effective search space used: 9497129280  
T: 11  
A: 40  
X1: 16 ( 7.4 bits)  
X2: 38 (14.6 bits)  
X3: 64 (24.7 bits)  
S1: 41 (21.9 bits)  
S2: 66 (30.0 bits)